

Additional file 1: Table S1. Accession numbers of IAP amino acid sequences used to perform multiple sequence alignment and generate a phylogenetic tree displayed in Figure 2.

Ticks species	Accession number
<i>Amblyomma sculptum</i>	JAT99717.1
<i>Amblyomma aureolatum</i>	JAT95460.1
<i>Amblyomma maculatum</i>	MCL6769568.1
<i>Amblyomma triste</i>	JAC33924.1
<i>Dermacentor reticulatus</i>	MBD2901002.1
<i>Hyalomma excavatum</i>	JAP65768.1
<i>Ixodes ricinus</i>	AR90216.1
<i>Ixodes scapularis</i>	MOY37746.1
<i>Ornithodoros erraticus</i>	MBZ3995776.1
<i>Ornithodoros moubata</i>	MBZ3985256.1
<i>Ornithodoros turicata</i>	MBY04351.1
<i>Rhipicephalus appendiculatus</i>	JAP78245.1
<i>Rhipicephalus microplus</i>	NOV33869.1
<i>Rhipicephalus pulchellus</i>	JAA59147.1
<i>Rhipicephalus zambeziensis</i>	MAA20231.1